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#10

SEQUENCE LISTING

NOVARTIS PHARMA S.A.

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> 16655

<140> PCT/EP99/07378

<141> 1999-09-13

<150> EP98402255.8

<151> 1998-09-11

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

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cctgtcaaag ataatatattt gaaatttgat caaattaatc ataaatctcc tacttttgatt 180  
atgggtatat tgaatatgac tcctgattca tttagtgatg gtgggaaaca ttttgaaaaa 240  
gaactagata atattgtgaa gcaggcagag aaattagtca gtgagggtgc tacgattatt 300  
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<213> Candida albicans

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<221> CDS

<222> (1)..(2364)

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<221> gene

<222> (1)..(2364)

<223> gene CaNL256

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Ile Thr Gly Lys Asp Ala Trp Asn Arg Pro Thr Pro Gln Pro Ile Thr	
20 25 30	
ata tca tta tct ttc aat act gat ttc cat aag gca tcg gaa ttg gat	144
Ile Ser Leu Ser Phe Asn Thr Asp Phe His Lys Ala Ser Glu Leu Asp	
35 40 45	
aat ttg aaa tac tca att aat tat gct gtt att acc aga aat gta act	192
Asn Leu Lys Tyr Ser Ile Asn Tyr Ala Val Ile Thr Arg Asn Val Thr	
50 55 60	
gaa ttt atg aaa tca aat gag cat tta aat ttc aag tca tta gga aat	240
Glu Phe Met Lys Ser Asn Glu His Leu Asn Phe Lys Ser Leu Gly Asn	
65 70 75 80	
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Ile Ala Gln Ala Ile Ser Asp Ile Gly Leu Asp Gln Ser Arg Gly Gly	
85 90 95	
gga tct att gtg gat gtg acg ata aaa agt ttg aaa tca gaa ata aga	336
Gly Ser Ile Val Asp Val Thr Ile Lys Ser Leu Lys Ser Glu Ile Arg	
100 105 110	
gct gaa agt gtc gaa tat aaa att aat aga aac act ttg ggt caa ccc	384
Ala Glu Ser Val Glu Tyr Lys Ile Asn Arg Asn Thr Leu Gly Gln Pro	
115 120 125	
gtt cca tta gat att ttc caa gtt aat aaa ttg aga tta ttg acg att	432
Val Pro Leu Asp Ile Phe Gln Val Asn Lys Leu Arg Leu Leu Thr Ile	
130 135 140	
att gga gtt ttc aca ttt gaa aga tta caa aaa caa ata gtt gat gtt	480
Ile Gly Val Phe Thr Phe Glu Arg Leu Gln Lys Gln Ile Val Asp Val	
145 150 155 160	
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Asp Leu Gln Phe Lys Ile Glu Pro Asn Ser Asn Leu Tyr Phe His Gln	
165 170 175	
ata att gct gat att gtt tca tac gtg gaa tca tct aat ttc aaa act	576
Ile Ile Ala Asp Ile Val Ser Tyr Val Glu Ser Ser Asn Phe Lys Thr	
180 185 190	
gta gaa gca ttg gtg tct aag att ggt caa ttg aca ttt cag aaa tat	624
Val Glu Ala Leu Val Ser Lys Ile Gly Gln Leu Thr Phe Gln Lys Tyr	
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210 215 220	

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225 230 235 240	
ttc aaa gat atg gaa cca gtt aaa ttt gaa aac aca att gct caa act	768
Phe Lys Asp Met Glu Pro Val Lys Phe Glu Asn Thr Ile Ala Gln Thr	
245 250 255	
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260 265 270	
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Thr Gly Tyr His Thr Ala Phe Ile Ala Phe Gly Ser Asn Thr Gly Asn	
275 280 285	
caa gta gaa aat att acc aat tca ttc gaa ttg ttg caa aaa tat gga	912
Gln Val Glu Asn Ile Thr Asn Ser Phe Glu Leu Leu Gln Lys Tyr Gly	
290 295 300	
atc acc ata gaa gca act tca tca ttg tac att tct aaa cca atg tat	960
Ile Thr Ile Glu Ala Thr Ser Ser Leu Tyr Ile Ser Lys Pro Met Tyr	
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tac ttg gat caa cca gat ttt ttc aat gga gta att aaa gtg aat ttc	1008
Tyr Leu Asp Gln Pro Asp Phe Phe Asn Gly Val Ile Lys Val Asn Phe	
325 330 335	
caa aac att tca cct ttc cag ttg ttg aaa att cta aaa gat att gaa	1056
Gln Asn Ile Ser Pro Phe Gln Leu Leu Lys Ile Leu Lys Asp Ile Glu	
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Tyr Lys His Leu Glu Arg Lys Lys Asp Phe Asp Asn Gly Pro Arg Ser	
355 360 365	
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Asn Leu Ile Ile Pro His Lys Ser Met Leu Glu Arg Thr Phe Val Leu	
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Gln Pro Leu Cys Glu Val Leu Pro Pro Asp Tyr Ile His Pro Ile Ser	
405 410 415	
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Ala Glu Ser Leu His Ser His Leu Gln Gln Leu Ile Asn Asp Lys Pro	
420 425 430	
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Gln Glu Thr Val Gln Glu Ser Ser Asp Leu Leu Gln Phe Ile Pro Val	-
435 440 445	
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His	Lys	Ser	Pro	Thr	Leu	Ile	Met	Gly	Ile	Leu	Asn	Met	Thr	Pro	Asp	
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Val	Lys	Gln	Ala	Glu	Lys	Leu	Val	Ser	Glu	Gly	Ala	Thr	Ile	Ile	Asp	
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gaa	gaa	ttg	gaa	cgt	gtg	att	cca	tta	att	aaa	gct	att	cgt	caa	tca	1632
Glu	Glu	Leu	Glu	Arg	Val	Ile	Pro	Leu	Ile	Lys	Ala	Ile	Arg	Gln	Ser	
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Leu	Asn	Pro	Asp	Leu	Leu	Lys	Val	Leu	Ile	Ser	Val	Asp	Thr	Tyr	Arg	
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Asp	Ile	Ser	Met	Gly	Lys	Tyr	Asp	Glu	Lys	Ile	Phe	Asp	Val	Val	Ala	
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Lys	Tyr	Gly	Cys	Pro	Tyr	Ile	Met	Asn	His	Thr	Arg	Gly	Ser	Pro	Lys	
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Thr	Met	Ser	Lys	Leu	Thr	Asn	Tyr	Glu	Ser	Asn	Thr	Asn	Asp	Asp	Ile	
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Ser	Pro	Glu	Ile	Lys	Asn	Leu	Leu	Asn	Gly	Ile	Ser	Arg	Glu	Leu	Ser	
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Leu	Gln	Met	Phe	Lys	Ala	Met	Ala	Lys	Gly	Val	Lys	Lys	Trp	Gln	Ile	
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675

680

685

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aat gaa cgt gtt gat gat gtg aca atc aaa cat aaa tat tta agt ttt 2160  
 Asn Glu Arg Val Asp Asp Val Thr Ile Lys His Lys Tyr Leu Ser Phe  
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aat ggt gct tgt gtt ttg gtg ggg aca tca aga aag aag ttt ttg ggg 2208  
 Asn Gly Ala Cys Val Leu Val Gly Thr Ser Arg Lys Lys Phe Leu Gly  
 725 730 735

aca tta act ggt aat gaa gtg cct ctg gat cga gta ttt ggc act ggt 2256  
 Thr Leu Thr Gly Asn Glu Val Pro Leu Asp Arg Val Phe Gly Thr Gly  
 740 745 750

gca aca gtg tct gcg tgt att gaa caa aac act gat att gta aga gtt 2304  
 Ala Thr Val Ser Ala Cys Ile Glu Gln Asn Thr Asp Ile Val Arg Val  
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 His Asp Val Lys Glu Met Lys Asp Val Val Cys Ile Ser Asp Ala Ile  
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&lt;211&gt; 788

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 3

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Ile Ser Leu Ser Phe Asn Thr Asp Phe His Lys Ala Ser Glu Leu Asp  
 35 40 45

Asn Leu Lys Tyr Ser Ile Asn Tyr Ala Val Ile Thr Arg Asn Val Thr  
 50 55 60

Glu Phe Met Lys Ser Asn Glu His Leu Asn Phe Lys Ser Leu Gly Asn  
 65 70 75 80

Ile Ala Gln Ala Ile Ser Asp Ile Gly Leu Asp Gln Ser Arg Gly Gly  
 85 90 95

Gly Ser Ile Val Asp Val Thr Ile Lys Ser Leu Lys Ser Glu Ile Arg  
 100 105 110

Ala Glu Ser Val Glu Tyr Lys Ile Asn Arg Asn Thr Leu Gly Gln Pro  
 115 120 125  
 Val Pro Leu Asp Ile Phe Gln Val Asn Lys Leu Arg Leu Leu Thr Ile  
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 Ile Gly Val Phe Thr Phe Glu Arg Leu Gln Lys Gln Ile Val Asp Val  
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 Asp Leu Gln Phe Lys Ile Glu Pro Asn Ser Asn Leu Tyr Phe His Gln  
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 180 185 190  
 Val Glu Ala Leu Val Ser Lys Ile Gly Gln Leu Thr Phe Gln Lys Tyr  
 195 200 205  
 Asp Gly Val Ala Glu Val Val Ala Thr Val Thr Lys Pro Asn Ala Phe  
 210 215 220  
 Ser His Val Glu Gly Val Gly Val Ser Ser Thr Met Val Lys Asp Asn  
 225 230 235 240  
 Phe Lys Asp Met Glu Pro Val Lys Phe Glu Asn Thr Ile Ala Gln Thr  
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 Asn Arg Ala Phe Asn Leu Pro Val Glu Asn Glu Lys Thr Glu Asp Tyr  
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 Thr Gly Tyr His Thr Ala Phe Ile Ala Phe Gly Ser Asn Thr Gly Asn  
 275 280 285  
 Gln Val Glu Asn Ile Thr Asn Ser Phe Glu Leu Leu Gln Lys Tyr Gly  
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 Ile Thr Ile Glu Ala Thr Ser Ser Leu Tyr Ile Ser Lys Pro Met Tyr  
 305 310 315 320  
 Tyr Leu Asp Gln Pro Asp Phe Phe Asn Gly Val Ile Lys Val Asn Phe  
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 340 345 350  
 Tyr Lys His Leu Glu Arg Lys Lys Asp Phe Asp Asn Gly Pro Arg Ser  
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 Ile Asp Leu Asp Ile Ile Leu Tyr Asp Asp Leu Gln Leu Asn Thr Glu  
 370 375 380  
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 385 390 395 400  
 Gln Pro Leu Cys Glu Val Leu Pro Pro Asp Tyr Ile His Pro Ile Ser  
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Ala Glu Ser Leu His Ser His Leu Gln Gln Leu Ile Asn Asp Lys Pro  
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 Gln Glu Thr Val Gln Glu Ser Ser Asp Leu Leu Gln Phe Ile Pro Val  
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 Ser Arg Leu Pro Val Lys Asp Asn Ile Leu Lys Phe Asp Gln Ile Asn  
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 His Lys Ser Pro Thr Leu Ile Met Gly Ile Leu Asn Met Thr Pro Asp  
 465 470 475 480  
 Ser Phe Ser Asp Gly Gly Lys His Phe Gly Lys Glu Leu Asp Asn Thr  
 485 490 495  
 Val Lys Gln Ala Glu Lys Leu Val Ser Glu Gly Ala Thr Ile Ile Asp  
 500 505 510  
 Ile Gly Gly Val Ser Thr Arg Pro Gly Ser Val Glu Pro Thr Glu Glu  
 515 520 525  
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 Leu Asn Pro Asp Leu Leu Lys Val Leu Ile Ser Val Asp Thr Tyr Arg  
 545 550 555 560  
 Arg Asn Val Ala Glu Gln Ser Leu Leu Val Gly Ala Asp Ile Ile Asn  
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 580 585 590  
 Lys Tyr Gly Cys Pro Tyr Ile Met Asn His Thr Arg Gly Ser Pro Lys  
 595 600 605  
 Thr Met Ser Lys Leu Thr Asn Tyr Glu Ser Asn Thr Asn Asp Asp Ile  
 610 615 620  
 Ile Glu Tyr Ile Ile Asp Pro Lys Leu Gly His Gln Glu Leu Asp Leu  
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 Ser Pro Glu Ile Lys Asn Leu Leu Asn Gly Ile Ser Arg Glu Leu Ser  
 645 650 655  
 Leu Gln Met Phe Lys Ala Met Ala Lys Gly Val Lys Lys Trp Gln Ile  
 660 665 670  
 Ile Leu Asp Pro Gly Ile Gly Phe Ala Lys Asn Leu Asn Gln Asn Leu  
 675 680 685  
 Ala Val Ile Arg Asn Ala Ser Phe Phe Lys Lys Tyr Ser Ile Gln Ile  
 690 695 700  
 Asn Glu Arg Val Asp Asp Val Thr Ile Lys His Lys Tyr Leu Ser Phe  
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Asn Gly Ala Cys Val Leu Val Gly Thr Ser Arg Lys Lys Phe Leu Gly  
725 730 735

Thr Leu Thr Gly Asn Glu Val Pro Leu Asp Arg Val Phe Gly Thr Gly  
740 745 750

Ala Thr Val Ser Ala Cys Ile Glu Gln Asn Thr Asp Ile Val Arg Val  
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Tyr Lys Asn Val  
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Probe

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aatgtgggga attggaaacc aagttatcca actcatttat ttatatttaa tgatttaatt 240  
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ggtggttcaa aatcgagatt acaagcgggt caatgttggc ccttaactca agtatcatta 360  
caacaaatca aatcaccgaa aaaagatgac gataagatgt attttatcaa tcttaaatcc 420  
aaatctttaa gttatgtata cctgacggat cgttatgatc attttgtgaa agttacggaa 480  
gcatttaata aaggtagaaa tgaaatgatt caaagtgaag gattattaga ttcaagactt 540  
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<212> DNA

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<222> (1)..(2373)



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aac agg aaa agc agg gct gta tgg cag aat aac aac act tct act cat	96
Asn Arg Lys Ser Arg Ala-Val Trp Gln Asn Asn Asn Thr Ser Thr His	
20 25 30	
aat aat cct tat gct aat tta agc act ggt gaa aaa agt agg agt cgc	144
Asn Asn Pro Tyr Ala Asn Leu Ser Thr Gly Glu Lys Ser Arg Ser Arg	
35 40 45	
cat aac act ggt agt tct tat gtt tct cca tat ggc ggc ggt aat gga	192
His Asn Thr Gly Ser Ser Tyr Val Ser Pro Tyr Gly Gly Gly Asn Gly	
50 55 60	
gag gag aat gct tat act ggg aat aac aac aaa tca aat act agt ggt	240
Glu Glu Asn Ala Tyr Thr Gly Asn Asn Asn Lys Ser Asn Thr Ser Gly	
65 70 75 80	
aat tta tta caa gtt cct gga gca gga gga gga gga gat ttg aat tct	288
Asn Leu Leu Gln Val Pro Gly Ala Gly Gly Gly Gly Asp Leu Asn Ser	
85 90 95	
aat aag aaa caa agt cga aga atg agt att cat gta tca gct cgt caa	336
Asn Lys Lys Gln Ser Arg Arg Met Ser Ile His Val Ser Ala Arg Gln	
100 105 110	
cat gga aga tca ttt tca caa act ggt cca att gat atg gca aat tta	384
His Gly Arg Ser Phe Ser Gln Thr Gly Pro Ile Asp Met Ala Asn Leu	
115 120 125	
ccg gca tta cct aaa ata ggt ggt gtt act act agt ggt gtt ggc ggt	432
Pro Ala Leu Pro Lys Ile Gly Gly Val Thr Thr Ser Gly Val Gly Gly	
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gct ggt ggt gat gtt atg aca agg act ggg gga ttg acg ata gaa caa	480
Ala Gly Gly Asp Val Met Thr Arg Thr Gly Gly Leu Thr Ile Glu Gln	
145 150 155 160	
aaa ata ttc aaa gaa tta agt caa gga tca gca gct gaa gtt gat gat	528
Lys Ile Phe Lys Glu Leu Ser Gln Gly Ser Ala Ala Glu Val Asp Asp	
165 170 175	
tat tac aag aca tta ttg aaa cag aaa aat tta atc act cgt gac att	576
Tyr Tyr Lys Thr Leu Leu Lys Gln Lys Asn Leu Ile Thr Arg Asp Ile	
180 185 190	
aag gat aat att aat cag aat caa aaa aat att tta caa tta aca aaa	624
Lys Asp Asn Ile Asn Gln Asn Gln Lys Asn Ile Leu Gln Leu Thr Lys	

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aga tta gaa ttg gaa ttt gaa cca gaa aca caa aaa gaa ctt cat ctg Arg Leu Glu Leu Glu Phe Glu Pro Glu Thr Gln Lys Glu Leu His Leu 245 250 255			768
cct caa aaa agt aat caa ttg ggt att cct agt aat aaa aag aaa gat Pro Gln Lys Ser Asn Gln Leu Gly Ile Pro Ser Asn Lys Lys Lys Asp 260 265 270			816
cga tca tca att atg gtg ctt aaa aaa atg tgg gat tct caa tta caa Arg Ser Ser Ile Met Val Leu Lys Lys Met Trp Asp Ser Gln Leu Gln 275 280 285			864
tca tta ttt aaa cat gtt gac ggt gca tca aaa ttt gtc caa cca tta Ser Leu Phe Lys His Val Asp Gly Ala Ser Lys Phe Val Gln Pro Leu 290 295 300			912
ccc aat aga cac att gtc gcg gaa agt gga cga tgg ttt gaa gtt aat Pro Asn Arg His Ile Val Ala Glu Ser Gly Arg Trp Phe Glu Val Asn 305 310 315 320			960
gtg ggg aat tgg aaa cca agt tat cca act cat tta ttt ata ttt aat Val Gly Asn Trp Lys Pro Ser Tyr Pro Thr His Leu Phe Ile Phe Asn 325 330 335			1008
gat tta att tta att act gtt aaa aaa tca tca tct agt agt cag gaa Asp Leu Ile Leu Ile Thr Val Lys Lys Ser Ser Ser Ser Ser Gln Glu 340 345 350			1056
cct act aca ggg gga agt aat ggt ggt tca aaa tcg aga tta caa gcg Pro Thr Thr Gly Gly Ser Asn Gly Gly Ser Lys Ser Arg Leu Gln Ala 355 360 365			1104
gtt caa tgt tgg ccc tta act caa gta tca tta caa caa atc aaa tca Val Gln Cys Trp Pro Leu Thr Gln Val Ser Leu Gln Gln Ile Lys Ser 370 375 380			1152
ccg aaa aaa gat gac gat aag atg tat ttt atc aat ctt aaa tcc aaa Pro Lys Lys Asp Asp Asp Lys Met Tyr Phe Ile Asn Leu Lys Ser Lys 385 390 395 400			1200
tct tta agt tat gta tac ctg acg gat cgt tat gat cat ttt gtg aaa Ser Leu Ser Tyr Val Tyr Leu Thr Asp Arg Tyr Asp His Phe Val Lys 405 410 415			1248
gtt acg gaa gca ttt aat aaa ggt aga aat gaa atg att caa agt gaa Val Thr Glu Ala Phe Asn Lys Gly Arg Asn Glu Met Ile Gln Ser Glu 420 425 430			1296

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435 440 445	
tct aaa gaa gag aaa cga caa tta cgg gaa tca tta aga aac tca ggc	1392
Ser Lys Glu Glu Lys Arg Gln Leu Arg Glu Ser Leu Arg Asn Ser Gly	
450 455 460	
aat tat aaa gaa gga gtt act gat gat gcc ggt gga gct gca act ggt	1440
Asn Tyr Lys Glu Gly Val Thr Asp Asp Ala Gly Gly Ala Ala Thr Gly	
465 470 475 480	
ggt ggt agg aaa agt gcc ggt act cct aat aga aat agt act gat tac	1488
Gly Gly Arg Lys Ser Ala Gly Thr Pro Asn Arg Asn Ser Thr Asp Tyr	
485 490 495	
gtt tta cat gat ata tct gct cga gta cat tca cgt aat cga tca caa	1536
Val Leu His Asp Ile Ser Ala Arg Val His Ser Arg Asn Arg Ser Gln	
500 505 510	
gat tta ggg aat aat ttc aaa tta gct aat aat ggg aaa tca caa ttt	1584
Asp Leu Gly Asn Asn Phe Lys Leu Ala Asn Asn Gly Lys Ser Gln Phe	
515 520 525	
ttc aat gaa atc aaa act tta gaa gat cga tta gat gat gtt gac gtt	1632
Phe Asn Glu Ile Lys Thr Leu Glu Asp Arg Leu Asp Asp Val Asp Val	
530 535 540	
gaa ata tcg cat aat caa tat gct gaa gcc gtg gaa tta ata tca ata	1680
Glu Ile Ser His Asn Gln Tyr Ala Glu Ala Val Glu Leu Ile Ser Ile	
545 550 555 560	
att gaa tct aaa tta cgt aat att gaa aat gca tta act aat caa cgt	1728
Ile Glu Ser Lys Leu Arg Asn Ile Glu Asn Ala Leu Thr Asn Gln Arg	
565 570 575	
aat gga ggt aaa aat gtc aat att gct gat gaa tta tta ctt tta gat	1776
Asn Gly Gly Lys Asn Val Asn Ile Ala Asp Glu Leu Leu Leu Leu Asp	
580 585 590	
gta tca aaa ttg aaa att aaa aat cgg aaa gaa aat gta tct aat gga	1824
Val Ser Lys Leu Lys Ile Lys Asn Arg Lys Glu Asn Val Ser Asn Gly	
595 600 605	
tta ata ttt gat tta caa cat aat ata gct aaa ctt aaa caa gat gat	1872
Leu Ile Phe Asp Leu Gln His Asn Ile Ala Lys Leu Lys Gln Asp Asp	
610 615 620	
att gat aat att ttg acg tta ttt gat aat tta gag caa tta gat cga	1920
Ile Asp Asn Ile Leu Thr Leu Phe Asp Asn Leu Glu Gln Leu Asp Arg	
625 630 635 640	
ggg gtt caa gga tat ttg gat tca atg tca gct tat tta tca act aca	1968
Gly Val Gln Gly Tyr Leu Asp Ser Met Ser Ala Tyr Leu Ser Thr Thr	
645 650 655	

gta tca aaa tta att gtt ggt tta caa gga tca acg aaa atc gat gtt 2016  
 Val Ser Lys Leu Ile Val Gly Leu Gln Gly Ser Thr Lys Ile Asp Val  
 660 665 670

gtt aat tat ctt tcc aat tta atg gtt att aat gta tcg att gtg aaa 2064  
 Val Asn Tyr Leu Ser Asn Leu Met Val Ile Asn Val Ser Ile Val Lys  
 675 680 685

cgt aca att caa act tat gaa caa ata att gct cca att tta aaa cgt 2112  
 Arg Thr Ile Gln Thr Tyr Glu Gln Ile Ile Ala Pro Ile Leu Lys Arg  
 690 695 700

cat ggt gat gtt gat tca agt gga ttg att aat tgg tgt att gat gaa 2160  
 His Gly Asp Val Asp Ser Ser Gly Leu Ile Asn Trp Cys Ile Asp Glu  
 705 710 715 720

ttt act aaa ctt tgt aaa caa att aaa aaa cat ttg tat gga aca ttg 2208  
 Phe Thr Lys Leu Cys Lys Gln Ile Lys Lys His Leu Tyr Gly Thr Leu  
 725 730 735

ttg ata tct tct ggg att aat atg gaa act gat gaa cca att tat aaa 2256  
 Leu Ile Ser Ser Gly Ile Asn Met Glu Thr Asp Glu Pro Ile Tyr Lys  
 740 745 750

gtt aaa gaa aga aaa tta tat gat aat ttc ttg aag att atg caa cca 2304  
 Val Lys Glu Arg Lys Leu Tyr Asp Asn Phe Leu Lys Ile Met Gln Pro  
 755 760 765

caa ttg gaa gaa tta aaa ctg gtg gga tta aat gtt gat tat ata ttt 2352  
 Gln Leu Glu Glu Leu Lys Leu Val Gly Leu Asn Val Asp Tyr Ile Phe  
 770 775 780

gag tct ata tta aat ctt gaa 2373  
 Glu Ser Ile Leu Asn Leu Glu  
 785 790

<210> 6

<211> 791

<212> PRT

<213> Candida albicans

<400> 6

Met Asp Asn Leu Asp Pro Asn Ser Ser Leu Gln Val Glu Lys Leu Arg  
 1 5 10 15

Asn Arg Lys Ser Arg Ala Val Trp Gln Asn Asn Asn Thr Ser Thr His  
 20 25 30

Asn Asn Pro Tyr Ala Asn Leu Ser Thr Gly Glu Lys Ser Arg Ser Arg  
 35 40 45

His Asn Thr Gly Ser Ser Tyr Val Ser Pro Tyr Gly Gly Gly Asn Gly  
 50 55 60

Glu Glu Asn Ala Tyr Thr Gly Asn Asn Asn Lys Ser Asn Thr Ser Gly  
 65 70 75 80

Asn Leu Leu Gln Val Pro Gly Ala Gly Gly Gly Gly Asp Leu Asn Ser  
                     85                    90                    95

Asn Lys Lys Gln Ser Arg Arg Met Ser Ile His Val Ser Ala Arg Gln  
                     100                    105                    110

His Gly Arg Ser Phe Ser Gln Thr Gly Pro Ile Asp Met Ala Asn Leu  
                     115                    120                    125

Pro Ala Leu Pro Lys Ile Gly Gly Val Thr Thr Ser Gly Val Gly Gly  
                     130                    135-                    140

Ala Gly Gly Asp Val Met Thr Arg Thr Gly Gly Leu Thr Ile Glu Gln  
                     145                    150                    155                    160

Lys Ile Phe Lys Glu Leu Ser Gln Gly Ser Ala Ala Glu Val Asp Asp  
                     165                    170                    175

Tyr Tyr Lys Thr Leu Leu Lys Gln Lys Asn Leu Ile Thr Arg Asp Ile  
                     180                    185                    190

Lys Asp Asn Ile Asn Gln Asn Gln Lys Asn Ile Leu Gln Leu Thr Lys  
                     195                    200                    205

Asp Leu Lys Glu Thr Gln Glu Glu Leu Ile Glu Leu Arg Gly Thr Thr  
                     210                    215                    220

Lys Glu Leu Tyr Glu Val Leu Gly Tyr Phe Lys Glu Ser Ala Gln Arg  
                     225                    230                    235                    240

Arg Leu Glu Leu Glu Phe Glu Pro Glu Thr Gln Lys Glu Leu His Leu  
                     245                    250                    255

Pro Gln Lys Ser Asn Gln Leu Gly Ile Pro Ser Asn Lys Lys Lys Asp  
                     260                    265                    270

Arg Ser Ser Ile Met Val Leu Lys Lys Met Trp Asp Ser Gln Leu Gln  
                     275                    280                    285

Ser Leu Phe Lys His Val Asp Gly Ala Ser Lys Phe Val Gln Pro Leu  
                     290                    295                    300

Pro Asn Arg His Ile Val Ala Glu Ser Gly Arg Trp Phe Glu Val Asn  
                     305                    310                    315                    320

Val Gly Asn Trp Lys Pro Ser Tyr Pro Thr His Leu Phe Ile Phe Asn  
                     325                    330                    335

Asp Leu Ile Leu Ile Thr Val Lys Lys Ser Ser Ser Ser Ser Gln Glu  
                     340                    345                    350

Pro Thr Thr Gly Gly Ser Asn Gly Gly Ser Lys Ser Arg Leu Gln Ala  
                     355                    360                    365

Val Gln Cys Trp Pro Leu Thr Gln Val Ser Leu Gln Gln Ile Lys Ser  
                     370                    375                    380

Pro Lys Lys Asp Asp Asp Lys Met Tyr Phe Ile Asn Leu Lys Ser Lys  
 385 390 395 400  
 Ser Leu Ser Tyr Val Tyr Leu Thr Asp Arg Tyr Asp His Phe Val Lys  
 405 410 415  
 Val Thr Glu Ala Phe Asn Lys Gly Arg Asn Glu Met Ile Gln Ser Glu  
 420 425 430  
 Arg Leu Leu Asp Ser Arg Leu Ser Ser Pro Ser Asn Asn Asn Gly Asp  
 435 440 445  
 Ser Lys Glu Glu Lys Arg Gln Leu Arg Glu Ser Leu Arg Asn Ser Gly  
 450 455 460  
 Asn Tyr Lys Glu Gly Val Thr Asp Asp Ala Gly Gly Ala Ala Thr Gly  
 465 470 475 480  
 Gly Gly Arg Lys Ser Ala Gly Thr Pro Asn Arg Asn Ser Thr Asp Tyr  
 485 490 495  
 Val Leu His Asp Ile Ser Ala Arg Val His Ser Arg Asn Arg Ser Gln  
 500 505 510  
 Asp Leu Gly Asn Asn Phe Lys Leu Ala Asn Asn Gly Lys Ser Gln Phe  
 515 520 525  
 Phe Asn Glu Ile Lys Thr Leu Glu Asp Arg Leu Asp Asp Val Asp Val  
 530 535 540  
 Glu Ile Ser His Asn Gln Tyr Ala Glu Ala Val Glu Leu Ile Ser Ile  
 545 550 555 560  
 Ile Glu Ser Lys Leu Arg Asn Ile Glu Asn Ala Leu Thr Asn Gln Arg  
 565 570 575  
 Asn Gly Gly Lys Asn Val Asn Ile Ala Asp Glu Leu Leu Leu Leu Asp  
 580 585 590  
 Val Ser Lys Leu Lys Ile Lys Asn Arg Lys Glu Asn Val Ser Asn Gly  
 595 600 605  
 Leu Ile Phe Asp Leu Gln His Asn Ile Ala Lys Leu Lys Gln Asp Asp  
 610 615 620  
 Ile Asp Asn Ile Leu Thr Leu Phe Asp Asn Leu Glu Gln Leu Asp Arg  
 625 630 635 640  
 Gly Val Gln Gly Tyr Leu Asp Ser Met Ser Ala Tyr Leu Ser Thr Thr  
 645 650 655  
 Val Ser Lys Leu Ile Val Gly Leu Gln Gly Ser Thr Lys Ile Asp Val  
 660 665 670  
 Val Asn Tyr Leu Ser Asn Leu Met Val Ile Asn Val Ser Ile Val Lys  
 675 680 685

Arg Thr Ile Gln Thr Tyr Glu Gln Ile Ile Ala Pro Ile Leu Lys Arg  
690 695 700

His Gly Asp Val Asp Ser Ser Gly Leu Ile Asn Trp Cys Ile Asp Glu  
705 710 715 720

Phe Thr Lys Leu Cys Lys Gln Ile Lys Lys His Leu Tyr Gly Thr Leu  
725 730 735

Leu Ile Ser Ser Gly Ile Asn Met Glu Thr Asp Glu Pro Ile Tyr Lys  
740 745 750

Val Lys Glu Arg Lys Leu Tyr Asp Asn Phe Leu Lys Ile Met Gln Pro  
755 760 765

Gln Leu Glu Glu Leu Lys Leu Val Gly Leu Asn Val Asp Tyr Ile Phe  
770 775 780

Glu Ser Ile Leu Asn Leu Glu  
785 790

<210> 7

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

<400> 7

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ttggtggttg ggtgtgtgtg gtccataagt atgccgtgtt gtcaccaccc ccagtcaata 120  
ccattggcaa tttaggatgt gaaaaaatag taaatatact atcggtatgt ttatcaaaat 180  
aagtccatga attgttgac atgtcaattt cttaaagtctc atgctcatca tctaattcca 240  
tctctcatc ttcttcacg ggtggcgctt gatcatcatc tgcaacttcc tcagccactt 300  
cattaacatt gatataattt tcttgagtat cgtctacgac gtc 343

<210> 8

<211> 1248

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(1245)

<220>

<221> gene

<222> (1)..(1245)

<223> gene CaIR012

<400> 8

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Met Ser His Gln Gln Glu Asp Val Val Asp Asp Thr Gln Glu Glu Tyr	
1 5 10 15	
atc aat gtt aat gaa gtg gct gag gaa gtt gca gat gat gat caa gcg	96
Ile Asn Val Asn Glu Val Ala Glu Glu Val Ala Asp Asp Asp Gln Ala	
20 25 30	
cca ccc gat gaa gaa gat gag gag atg gaa tta gat gat gag cat gag	144
Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu	
35 40 45	
act tta gaa att gac atg tcc aac aat tca tgg act tat ttt gat aaa	192
Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys	
50 55 60	
cat acc gat agt ata ttt act att ttt tca cat cct aaa ttg cca atg	240
His Thr Asp Ser Ile Phe Thr Ile Phe Ser His Pro Lys Leu Pro Met	
65 70 75 80	
gta ttg act ggg ggt ggt gac aac acg gca tac tta tgg acc aca cac	288
Val Leu Thr Gly Gly Gly Asp Asn Thr Ala Tyr Leu Trp Thr Thr His	
85 90 95	
acc caa cca cca aga ttt gtt ggc gaa atc act gga cat aaa gag tct	336
Thr Gln Pro Pro Arg Phe Val Gly Glu Ile Thr Gly His Lys Glu Ser	
100 105 110	
gtt ata tct gga ggg ttt act gca gac ggc aag ttt gtt gtt act gca	384
Val Ile Ser Gly Gly Phe Thr Ala Asp Gly Lys Phe Val Val Thr Ala	
115 120 125	
gac atg aat gga tta att caa gtt ttc aaa gcc aca aaa gga ggt gaa	432
Asp Met Asn Gly Leu Ile Gln Val Phe Lys Ala Thr Lys Gly Gly Glu	
130 135 140	
cag tgg gtg aaa ttt ggt gaa ttg gac gaa gtt gaa gaa gtg ttg ttt	480
Gln Trp Val Lys Phe Gly Glu Leu Asp Glu Val Glu Glu Val Leu Phe	
145 150 155 160	
gtt act gtg cat cca aca tta cca ttc ttt gcc ttt ggt gct acc gat	528
Val Thr Val His Pro Thr Leu Pro Phe Phe Ala Phe Gly Ala Thr Asp	
165 170 175	
gga tct ata tgg gtc tac caa ata gac gaa tcc agt aaa ctg cta gtg	576
Gly Ser Ile Trp Val Tyr Gln Ile Asp Glu Ser Ser Lys Leu Leu Val	
180 185 190	
caa att atg tct ggg ttc tca cac aca tta gaa tgt aat ggt gct gta	624
Gln Ile Met Ser Gly Phe Ser His Thr Leu Glu Cys Asn Gly Ala Val	
195 200 205	
ttt ata caa gga aaa gat gaa aat gat ttg aca ttg gtc tct ata agt	672
Phe Ile Gln Gly Lys Asp Glu Asn Asp Leu Thr Leu Val Ser Ile Ser	



210	215	220	
gaa gat ggt act gtg	gtg aac tgg aac tgt ttt	aca gga caa gtg aat	720
Glu Asp Gly Thr Val	Val Asn Trp Asn Cys	Phe Thr Gly Gln Val Asn	
225	230	235 240	
tat aaa ttg caa cct cat	gat gac ttt aaa gga gtt	gaa agt ccg tgg	768
Tyr Lys Leu Gln Pro	His Asp Asp Phe Lys	Gly Val Glu Ser Pro Trp	
	245	250 255	
gtc acg gtc aaa gta cat	ggt aat ctt gtg gcc att	ggt ggc aga gat	816
Val Thr Val Lys Val	His Gly Asn Leu Val	Ala Ile Gly Gly Arg Asp	
	260	265 270	
ggc cag cta tca att gtg	aac aat gac act ggt	aaa atc gtt cat act	864
Gly Gln Leu Ser Ile	Val Asn Asn Asp Thr	Gly Lys Ile Val His Thr	
	275	280 285	
ctt aaa aca ttg gat aat	gtc gac gac att gca	gaa ctc tca att gag	912
Leu Lys Thr Leu Asp	Asn Val Asp Asp Ile	Ala Glu Leu Ser Ile Glu	
	290	295 300	
gca ttg agt tgg tgt gaa	agc aaa aat att aac	ctc ttg gca gtg ggt	960
Ala Leu Ser Trp Cys	Glu Ser Lys Asn Ile	Asn Leu Leu Ala Val Gly	
305	310	315 320	
ttg gtt tct ggt gac gtt	tta tta ttt gat act	cag caa tgg aga ttg	1008
Leu Val Ser Gly Asp	Val Leu Leu Phe Asp	Thr Gln Gln Trp Arg Leu	
	325	330 335	
aga aag aac ttg aaa gtt	gac gat gcc atc acc	aaa tta caa ttt gtt	1056
Arg Lys Asn Leu Lys	Val Asp Asp Ala Ile	Thr Lys Leu Gln Phe Val	
	340	345 350	
ggc gaa acc ccc att ttg	gtg gga agt agt atg	gat ggt aaa att tac	1104
Gly Glu Thr Pro Ile	Leu Val Gly Ser Ser	Met Asp Gly Lys Ile Tyr	
	355	360 365	
aaa tgg gac gct aga act	ggt gaa gag ttg ttt	gct ggt gtg gga cac	1152
Lys Trp Asp Ala Arg	Thr Gly Glu Glu Leu	Phe Ala Gly Val Gly His	
	370	375 380	
aac atg gga gta ttg gac	ttt gct att tta gat	gga ggt aaa aag ttg	1200
Asn Met Gly Val Leu	Asp Phe Ala Ile Leu	Asp Gly Gly Lys Lys Leu	
385	390	395 400	
gtt act gct ggt gat gaa	ggt gtt tca ttg gtc	ttt gta cat gaa tag	1248
Val Thr Ala Gly Asp	Glu Gly Val Ser Leu	Val Phe Val His Glu	
	405	410 415	

<210> 9

<211> 415

<212> PRT

<213> Candida albicans

<400> 9

Met Ser His Gln Gln Glu Asp Val Val Asp Asp Thr Gln Glu Glu Tyr  
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 Ile Asn Val Asn Glu Val Ala Glu Glu Val Ala Asp Asp Asp Gln Ala  
 20 25 30  
 Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu  
 35 40 45  
 Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys  
 50 55 60  
 His Thr Asp Ser Ile Phe Thr Ile Phe Ser His Pro Lys Leu Pro Met  
 65 70 75 80  
 Val Leu Thr Gly Gly Gly Asp Asn Thr Ala Tyr Leu Trp Thr Thr His  
 85 90 95  
 Thr Gln Pro Pro Arg Phe Val Gly Glu Ile Thr Gly His Lys Glu Ser  
 100 105 110  
 Val Ile Ser Gly Gly Phe Thr Ala Asp Gly Lys Phe Val Val Thr Ala  
 115 120 125  
 Asp Met Asn Gly Leu Ile Gln Val Phe Lys Ala Thr Lys Gly Gly Glu  
 130 135 140  
 Gln Trp Val Lys Phe Gly Glu Leu Asp Glu Val Glu Glu Val Leu Phe  
 145 150 155 160  
 Val Thr Val His Pro Thr Leu Pro Phe Phe Ala Phe Gly Ala Thr Asp  
 165 170 175  
 Gly Ser Ile Trp Val Tyr Gln Ile Asp Glu Ser Ser Lys Leu Leu Val  
 180 185 190  
 Gln Ile Met Ser Gly Phe Ser His Thr Leu Glu Cys Asn Gly Ala Val  
 195 200 205  
 Phe Ile Gln Gly Lys Asp Glu Asn Asp Leu Thr Leu Val Ser Ile Ser  
 210 215 220  
 Glu Asp Gly Thr Val Val Asn Trp Asn Cys Phe Thr Gly Gln Val Asn  
 225 230 235 240  
 Tyr Lys Leu Gln Pro His Asp Asp Phe Lys Gly Val Glu Ser Pro Trp  
 245 250 255  
 Val Thr Val Lys Val His Gly Asn Leu Val Ala Ile Gly Gly Arg Asp  
 260 265 270  
 Gly Gln Leu Ser Ile Val Asn Asn Asp Thr Gly Lys Ile Val His Thr  
 275 280 285  
 Leu Lys Thr Leu Asp Asn Val Asp Asp Ile Ala Glu Leu Ser Ile Glu  
 290 295 300

Ala Leu Ser Trp Cys Glu Ser Lys Asn Ile Asn Leu Leu Ala Val Gly  
305 310 315 320

Leu Val Ser Gly Asp Val Leu Leu Phe Asp Thr Gln Gln Trp Arg Leu  
325 330 335

Arg Lys Asn Leu Lys Val Asp Asp Ala Ile Thr Lys Leu Gln Phe Val  
340 345 350

Gly Glu Thr Pro Ile Leu Val Gly Ser Ser Met Asp Gly Lys Ile Tyr  
355 360 365

Lys Trp Asp Ala Arg Thr Gly Glu Glu Leu Phe Ala Gly Val Gly His  
370 375 380

Asn Met Gly Val Leu Asp Phe Ala Ile Leu Asp Gly Gly Lys Lys Leu  
385 390 395 400

Val Thr Ala Gly Asp Glu Gly Val Ser Leu Val Phe Val His Glu  
405 410 415

<210> 10

<211> 5544

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(5541)

<220>

<221> gene

<222> (1)..(5541)

<223> gene CaJL039

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Met Ser Gly Ile Phe Asn Trp Ser Leu Asp Val Phe Ala Asp Ile Tyr  
1 5 10 15

aac acc ctc aag ttt gag tcc aat ata gat ttg gat aca atc gac ttc 96  
Asn Thr Leu Lys Phe Glu Ser Asn Ile Asp Leu Asp Thr Ile Asp Phe  
20 25 30

acc agc atc aag aat gat ctt gca aat gtt ttg att aca cca gtc cct 144  
Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro  
35 40 45

ctg gat caa tca cgt agc aaa ctt gga gac gca tca aaa cca gtg gcg 192  
Leu Asp Gln Ser Arg Ser Lys Leu Gly Asp Ala Ser Lys Pro Val Ala  
50 55 60

ttg ccc agt gga gat gag gtg aaa ttg aat caa gca tca att gaa att 240  
Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile  
65 70 75 80

act gga gtt tta tca aat gaa ttg gat tta gat gaa cta aat aca gca	288
Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala	
85 90 95	
gag ttg tta tat aac gca agt gac ttg agc tac aag aag gga acg tcc	336
Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser	
100 105 110	
att ggc gat agt gct cga ttg gct tat tat tta aga gct cat tat ata	384
Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile	
115 120 125	
cta aac att gtt gga tac tta gtt tcg cat aaa cgt tta gat atc atc	432
Leu Asn Ile Val Gly Tyr Leu Val Ser His Lys Arg Leu Asp Ile Ile	
130 135 140	
act aac aac aac caa gtg ttg ttt gac aat att ttg aaa agt ttc agc	480
Thr Asn Asn Asn Gln Val Leu Phe Asp Asn Ile Leu Lys Ser Phe Ser	
145 150 155 160	
aag att tat act ttg agt ggt aaa tta aat gac atg att gac aag caa	528
Lys Ile Tyr Thr Leu Ser Gly Lys Leu Asn Asp Met Ile Asp Lys Gln	
165 170 175	
aaa gtt acc ggc gac atc aac aat ctt gca ttt atc aat tgt atc aat	576
Lys Val Thr Gly Asp Ile Asn Asn Leu Ala Phe Ile Asn Cys Ile Asn	
180 185 190	
tat tcc aga agt cag ttg ttt aat gca cac gag tta ttg gga caa gtt	624
Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val	
195 200 205	
gta ttt gga tta gcg gat aat tat tat gag agt tat ggc aca cta aac	672
Val Phe Gly Leu Ala Asp Asn Tyr Tyr Glu Ser Tyr Gly Thr Leu Asn	
210 215 220	
aac tat aat tcc tta gtg gag ttt ata ctg aaa aat atc agc gat gaa	720
Asn Tyr Asn Ser Leu Val Glu Phe Ile Leu Lys Asn Ile Ser Asp Glu	
225 230 235 240	
gat gtt ttt gtt atc cat ttt tta cca tcc act tta caa ttg ttc aag	768
Asp Val Phe Val Ile His Phe Leu Pro Ser Thr Leu Gln Leu Phe Lys	
245 250 255	
aaa tta ctt caa cta ggt gag gaa tct tta gtc gat cag ttt tac aag	816
Lys Leu Leu Gln Leu Gly Glu Glu Ser Leu Val Asp Gln Phe Tyr Lys	
260 265 270	
act ata acc tct tcc ata cta aaa gat tat gaa gcc aac aat ttt tcc	864
Thr Ile Thr Ser Ser Ile Leu Lys Asp Tyr Glu Ala Asn Asn Phe Ser	
275 280 285	
aaa agt gaa gat att gac ttg tca aaa tca aaa ttg tct ggc ttt gaa	912
Lys Ser Glu Asp Ile Asp Leu Ser Lys Ser Lys Leu Ser Gly Phe Glu	
290 295 300	
ata gtc aca agc ttt att ttt cta act gag ttt att cca tgg tgc aag	960

Ile Val Thr Ser Phe	Ile Phe Leu Thr Glu Phe Ile Pro Trp Cys Lys	
305	310 315	320
cag ctg tca agt aga acc gcg aaa tac gat ttc aaa gat gat ata tta		1008
Gln Leu Ser Ser Arg Thr Ala Lys Tyr Asp Phe Lys Asp Asp Ile Leu		
	325 330 335	
aag tat atg gaa ttc ttg ata agt tat gga gtt atg gaa cga tta tta		1056
Lys Tyr Met Glu Phe Leu Ile Ser Tyr Gly Val Met Glu Arg Leu Leu		
	340 345 350	
tca tac tgt tct gaa acc agc aat gca aaa act cag caa gtg tac gac		1104
Ser Tyr Cys Ser Glu Thr Ser Asn Ala Lys Thr Gln Gln Val Tyr Asp		
	355 360 365	
tgg tca aac atg tac gat ttc aga gca ttg ctt caa aag aat ttc cca		1152
Trp Ser Asn Met Tyr Asp Phe Arg Ala Leu Leu Gln Lys Asn Phe Pro		
	370 375 380	
cga ctt aca cca gca aaa ttt cat tat cct ggc aat caa gaa ttg ttg		1200
Arg Leu Thr Pro Ala Lys Phe His Tyr Pro Gly Asn Gln Glu Leu Leu		
	385 390 395 400	
aat gca gtt aga ccg gga tat gaa aat ata tcc aaa ttg att gac att		1248
Asn Ala Val Arg Pro Gly Tyr Glu Asn Ile Ser Lys Leu Ile Asp Ile		
	405 410 415	
tcc ttt ttg acg tta gat cca tcg ctt aat gag acg ttg gtt tca cct		1296
Ser Phe Leu Thr Leu Asp Pro Ser Leu Asn Glu Thr Leu Val Ser Pro		
	420 425 430	
ttt ttc cag agc ttt ttc agt gtg ttt ata tct aat gcc gca gtt gtt		1344
Phe Phe Gln Ser Phe Phe Ser Val Phe Ile Ser Asn Ala Ala Val Val		
	435 440 445	
atg acc tct tta agg gac tca gag gaa gat ttt gtt tta tcg tcg ttg		1392
Met Thr Ser Leu Arg Asp Ser Glu Glu Asp Phe Val Leu Ser Ser Leu		
	450 455 460	
aat gaa agt gac gaa gag gaa gaa gaa gaa gaa agc gac agc gac gaa		1440
Asn Glu Ser Asp Glu Glu Glu Glu Glu Glu Glu Ser Asp Ser Asp Glu		
	465 470 475 480	
gat tct tcg acc cca aaa aac aaa gaa aaa tca gct ggg tta gac ctt		1488
Asp Ser Ser Thr Pro Lys Asn Lys Glu Lys Ser Ala Gly Leu Asp Leu		
	485 490 495	
gac aag att gcc cag cgt gct gaa tta gaa agg ttc tac ttg gct ttc		1536
Asp Lys Ile Ala Gln Arg Ala Glu Leu Glu Arg Phe Tyr Leu Ala Phe		
	500 505 510	
gcg tac acc tac aac aat cga cct gaa ttg tgt gcg tta ttt tgg ggg		1584
Ala Tyr Thr Tyr Asn Asn Arg Pro Glu Leu Cys Ala Leu Phe Trp Gly		
	515 520 525	
aac gag cag gta act cat gac att ata gga ttt att tcc tgg gga ctt		1632
Asn Glu Gln Val Thr His Asp Ile Ile Gly Phe Ile Ser Trp Gly Leu		

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gct aat aat acg tct ccg ttg atc act gca aca ttc tgc tta cta tta			1680
Ala Asn Asn Thr Ser Pro Leu Ile Thr Ala Thr Phe Cys Leu Leu Leu			
545	550	555	560
ggg tcg ttg gca tct gct ggt gca gag gca act tca agg ata tgg gag			1728
Gly Ser Leu Ala Ser Ala Gly Ala Glu Ala Thr Ser Arg Ile Trp Glu			
	565	570	575
att ctt gta cac aac aat aac aac gca agt acg aga aaa aat gat ttt			1776
Ile Leu Val His Asn Asn Asn Asn Ala Ser Thr Arg Lys Asn Asp Phe			
	580	585	590
tca aag gta tcc gtt gac tcc ctt tat gat tcg ttg aaa tat tac att			1824
Ser Lys Val Ser Val Asp Ser Leu Tyr Asp Ser Leu Lys Tyr Tyr Ile			
	595	600	605
gac tct tta aat gaa agc ttt gaa caa gat tta aat gcc caa ttg atg			1872
Asp Ser Leu Asn Glu Ser Phe Glu Gln Asp Leu Asn Ala Gln Leu Met			
	610	615	620
ttg aat cag aag aaa caa gat ttt ctc ttc agc acc aca aca agc aaa			1920
Leu Asn Gln Lys Lys Gln Asp Phe Leu Phe Ser Thr Thr Thr Ser Lys			
	625	630	635
cag gac ctt gat gat tct ggc gag aat aga att gtt ata gag ttg gcc			1968
Gln Asp Leu Asp Asp Ser Gly Glu Asn Arg Ile Val Ile Glu Leu Ala			
	645	650	655
gag gat tca ctt gtc ctc att tca ggg ttt att caa tta ctt tct gca			2016
Glu Asp Ser Leu Val Leu Ile Ser Gly Phe Ile Gln Leu Leu Ser Ala			
	660	665	670
att gtg aag aat ttg aac act aag aat gaa aga agc aaa gaa atc aaa			2064
Ile Val Lys Asn Leu Asn Thr Lys Asn Glu Arg Ser Lys Glu Ile Lys			
	675	680	685
tcc gtg gta tac act aga ttc tca cca atc att aaa ggg ttt tta aaa			2112
Ser Val Val Tyr Thr Arg Phe Ser Pro Ile Ile Lys Gly Phe Leu Lys			
	690	695	700
ttc gat aat ttg atc aat ggt agc agg ttc ctt caa gtt gat gct agc			2160
Phe Asp Asn Leu Ile Asn Gly Ser Arg Phe Leu Gln Val Asp Ala Ser			
	705	710	715
att caa agc aca aac aac ccc aaa ttt att gat ttg cca aat gtt ttc			2208
Ile Gln Ser Thr Asn Asn Pro Lys Phe Ile Asp Leu Pro Asn Val Phe			
	725	730	735
gtc agt gat gac tcg aga att ata ttg acg aac ctc att cta acc ttt			2256
Val Ser Asp Asp Ser Arg Ile Ile Leu Thr Asn Leu Ile Leu Thr Phe			
	740	745	750
tta ggc gat ttt gtt acc aac gat agt gat ccg tat att aga tat gag			2304
Leu Gly Asp Phe Val Thr Asn Asp Ser Asp Pro Tyr Ile Arg Tyr Glu			
	755	760	765

att tgg cgt tta gtc gat cga tgg atg tac cag ggg ttg cat agt ttg Ile Trp Arg Leu Val Asp Arg Trp Met Tyr Gln Gly Leu His Ser Leu 770 775 780	2352
cca gaa gac aag aaa gat gat gct ttt aga cat att aag aga aag tat Pro Glu Asp Lys Lys Asp Asp Ala Phe Arg His Ile Lys Arg Lys Tyr 785 790 795 800	2400
aac agt aag aaa aat gtt ccc atc aat caa gca ttt tca aca aac cta Asn Ser Lys Lys Asn Val Pro Ile Asn Gln Ala Phe Ser Thr Asn Leu 805 810 815	2448
act cat ctt agt caa att ggg aat ttc act gtc ttg gtg aaa aaa ttg Thr His Leu Ser Gln Ile Gly Asn Phe Thr Val Leu Val Lys Lys Leu 820 825 830	2496
tta acc cca tat gca gat agt aat gaa gca ttc acc aag tac tcg ttg Leu Thr Pro Tyr Ala Asp Ser Asn Glu Ala Phe Thr Lys Tyr Ser Leu 835 840 845	2544
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gga att tgg cca tac att gaa ttt tta atg caa aat gtg ttt gca aat Gly Ile Trp Pro Tyr Ile Glu Phe Leu Met Gln Asn Val Phe Ala Asn 865 870 875 880	2640
tct ggt act att gct aat aaa cga gat agg gtc aac ttg caa ctt aat Ser Gly Thr Ile Ala Asn Lys Arg Asp Arg Val Asn Leu Gln Leu Asn 885 890 895	2688
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aaa gca att tcc ata ttg aaa gga gta agc caa tcc aag ttt ttt gtt Lys Ala Ile Ser Ile Leu Lys Gly Val Ser Gln Ser Lys Phe Phe Val 1090 1095 1100	3312
acc aga gtt tca agc tct gct gat ccc tta ctc aac aac gat aga ttg Thr Arg Val Ser Ser Ser Ala Asp Pro Leu Leu Asn Asn Asp Arg Leu 1105 1110 1115 1120	3360
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gag ata ttg gat ttt gtt ttg ggc aat ctc aat caa ttt gat ggc aaa Glu Ile Leu Asp Phe Val Leu Gly Asn Leu Asn Gln Phe Asp Gly Lys 1155 1160 1165	3504
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tac aat aat ggt aat aac cat att att gat gtt ggt cca gcc aag ctt	3696



Tyr Asn Asn Gly Asn Asn His Ile Ile Asp Val Gly Pro Ala Lys Leu	
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tcg tcg ttg att tta cag att ctt atc aag ttg tgc caa gat cca att	3744
Ser Ser Leu Ile Leu Gln Ile Leu Ile Lys Leu Cys Gln Asp Pro Ile	
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Ser Ser Ser Ile Thr Leu Asn Gln Leu Arg Glu Tyr Glu Glu Leu Phe	
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gaa aaa ttg gtt aac tgt caa cct aaa ctt gat ttg aat acc gtt tgg	3840
Glu Lys Leu Val Asn Cys Gln Pro Lys Leu Asp Leu Asn Thr Val Trp	
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Cys Gly Asn Gln Phe Asp Gly Asp Leu Gln Ile Asp Ala Ser Asn Val	
1285 1290 1295	
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Phe Val Asp Asn Gln Ala Ser Thr Gln Ala Phe Phe Ser Phe Ile Asn	
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Gln Arg Asn Leu Ile Leu Gln Tyr Leu Ser Leu Glu Phe His Ser Val	
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Lys Ser Arg Thr Lys Arg Glu Tyr Tyr Ser Lys Val Leu Thr Asn Asp	
1330 1335 1340	
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Lys Glu Phe Val Asn Arg Thr Pro Lys Val Leu Thr Phe Leu Asn Ile	
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Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu	

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Phe Val Arg Val Ala Lys Ser Lys Asn Gly Ala Leu Gln Leu Ile Gln	
1685 1690 1695	

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Asn Glu Leu Phe Ser Ile Leu His Gln Ser Lys Phe Leu Gln Ile Asp	
1700 1705 1710	

cca gat att ggt tta agt tta cga att gaa gaa gtt caa gat cac aag	5184
Pro Asp Ile Gly Leu Ser Leu Arg Ile Glu Glu Val Gln Asp His Lys	
1715 1720 1725	

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Thr Val Asn Val Asn Val Leu Leu Asp Thr Pro Leu Ser Ile Thr Asp	
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Glu Phe Leu Val Pro Ile Phe Gln Leu Leu Thr Thr Val Leu Leu Ser	
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Lys Ser Val Asn Arg Leu Val Val Gly Val Met Lys Arg Asp Phe Leu	
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Val Glu Thr Lys Gln Ile Gly Gln Gly Leu Tyr Lys Glu Glu Ser His	
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Glu Leu Val Ser Leu Lys Glu Leu Val Lys Leu Phe Ile Leu Ile Asp	
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<213> Candida albicans

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Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro  
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 Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile  
 65 70 75 80  
 Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala  
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 Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser  
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 Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile  
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 Leu Asn Ile Val Gly Tyr Leu Val Ser His Lys Arg Leu Asp Ile Ile  
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 Lys Val Thr Gly Asp Ile Asn Asn Leu Ala Phe Ile Asn Cys Ile Asn  
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 Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val  
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Lys Tyr Met Glu Phe Leu Ile Ser Tyr Gly Val Met Glu Arg Leu Leu  
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 Ser Tyr Cys Ser Glu Thr Ser Asn Ala Lys Thr Gln Gln Val Tyr Asp  
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Gln Asp Leu Asp Asp Ser Gly Glu Asn Arg Ile Val Ile Glu Leu Ala  
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 Glu Asp Ser Leu Val Leu Ile Ser Gly Phe Ile Gln Leu Leu Ser Ala  
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Phe Val Lys Leu His His Ser Val Ala Val Ile Asn Tyr Leu Phe Glu  
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Ser Ser Leu Ile Leu Gln Ile Leu Ile Lys Leu Cys Gln Asp Pro Ile  
1235 1240 1245

Ser Ser Ser Ile Thr Leu Asn Gln Leu Arg Glu Tyr Glu Glu Leu Phe  
 1250 1255 1260

Glu Lys Leu Val Asn Cys Gln Pro Lys Leu Asp Leu Asn Thr Val Trp  
 265 1270 1275 1280

Cys Gly Asn Gln Phe Asp Gly Asp Leu Gln Ile Asp Ala Ser Asn Val  
 1285 1290 1295

Phe Val Asp Asn Gln Ala Ser Thr Gln Ala Phe Phe Ser Phe Ile Asn  
 1300 1305 1310

Gln Arg Asn Leu Ile Leu Gln Tyr Leu Ser Leu Glu Phe His Ser Val  
 1315 1320 1325

Lys Ser Arg Thr Lys Arg Glu Tyr Tyr Ser Lys Val Leu Thr Asn Asp  
 1330 1335 1340

Lys Glu Phe Val Asn Arg Thr Pro Lys Val Leu Thr Phe Leu Asn Ile  
 345 1350 1355 1360

Leu Asn Tyr Ser Phe Lys Asn Phe Glu Val Gln Lys Tyr Glu Trp Leu  
 1365 1370 1375

Asp Gln Lys Phe Asn Val Ser Leu Leu Leu Ala Glu Val Asn Ala Gln  
 1380 1385 1390

Lys Asn Gly Thr Leu Asp Phe Ser Val Leu Thr Lys Val Phe Arg Leu  
 1395 1400 1405

Leu Cys Gln Thr Ser Asn Leu Ile Thr Pro Glu Ser Lys Gln Leu Phe  
 1410 1415 1420

Ala Glu Glu Ile Met Val Glu Gly Ser Lys Ile Ser Asp Phe Val Thr  
 425 1430 1435 1440

Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu  
 1445 1450 1455

His Ser Trp Cys Gln Leu Ile Glu Ile Leu Val Thr Asp Ser Gly Ile  
 1460 1465 1470

Asn Ser Leu Asn Phe Ile Leu Glu Val Leu Gln Val Ile Ile Pro Lys  
 1475 1480 1485

Ile Asn Asp Tyr Phe Asp Val Asp Ile Leu Phe Ser Glu Glu Met Val  
 1490 1495 1500

Ser Leu Cys Val Leu Leu Phe Asp Leu Tyr Asp Gln Leu Thr Leu Ala  
 505 1510 1515 1520

Asp Arg Lys Gly Glu Asp Phe Ala Leu Gly Ile Glu Arg Leu Ile Pro  
 1525 1530 1535

Leu Phe Gln Thr Cys Ile Ala Gly Ile Leu Asn Ser Asn Ser Thr Pro  
 1540 1545 1550



Ser Leu Arg Ser Asp Leu Tyr Val Val Gly Asn Lys Phe Leu Leu Lys  
 1555 1560 1565  
 Cys Phe Glu Arg Glu Ser Phe Leu Lys Gln Val Met His Ile Ile Lys  
 1570 1575 1580  
 Ser Val Asp Lys Lys Phe Phe Gln Val Ile Cys Asn Asp Ala Ile Tyr  
 585 1590 1595 1600  
 Ser Glu Gly Pro Ser Arg Ile Thr Ser Thr Leu Phe Leu Glu Ser Leu  
 1605 1610 1615  
 Val His Leu Gly Thr Leu Val Lys Val Asp Phe Ile Leu Asn Ala Leu  
 1620 1625 1630  
 Ile Lys Asn Asn Ala Leu Leu Leu Leu Val Arg Ser Val Lys Arg Thr  
 1635 1640 1645  
 Asp Ala Met Ile Lys Leu Cys Gln Glu Lys Asn Ser Gly Val Thr Leu  
 1650 1655 1660  
 Asp His Phe Ile Phe Asp Leu Met Ala Phe Lys Ala Thr Leu Tyr Phe  
 665 1670 1675 1680  
 Phe Val Arg Val Ala Lys Ser Lys Asn Gly Ala Leu Gln Leu Ile Gln  
 1685 1690 1695  
 Asn Glu Leu Phe Ser Ile Leu His Gln Ser Lys Phe Leu Gln Ile Asp  
 1700 1705 1710  
 Pro Asp Ile Gly Leu Ser Leu Arg Ile Glu Glu Val Gln Asp His Lys  
 1715 1720 1725  
 Thr Val Asn Val Asn Val Leu Leu Asp Thr Pro Leu Ser Ile Thr Asp  
 1730 1735 1740  
 Leu Val Asp Pro Tyr Lys Leu Arg Ser Glu Asn Thr Ile Ser Tyr Phe  
 745 1750 1755 1760  
 Glu Phe Leu Val Pro Ile Phe Gln Leu Leu Thr Thr Val Leu Leu Ser  
 1765 1770 1775  
 Met Gly Pro Asn Tyr Gln Pro Ala Ile Ile Gln Thr Arg Glu Leu Met  
 1780 1785 1790  
 Lys Ser Val Asn Arg Leu Val Val Gly Val Met Lys Arg Asp Phe Leu  
 1795 1800 1805  
 Val Glu Thr Lys Gln Ile Gly Gln Gly Leu Tyr Lys Glu Glu Ser His  
 1810 1815 1820  
 Glu Leu Val Ser Leu Lys Glu Leu Val Lys Leu Phe Ile Leu Ile Asp  
 825 1830 1835 1840  
 Ser Leu Ala His Tyr Ser Val  
 1845

<210> 12  
<211> 575  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Probe

<400> 12  
gtttggtgac tcaacctacc accaatcgat ttacactctt cataagttct ctagtttgaa 60  
taattgcagg ttgataattt ggtcccattg acaataacac tggtgtaagt agctgaaata 120  
ttggtacaag gaactcaaaa tatgatatag tgttttcact tcgcaacttg tatggatcca 180  
ccaagtcagt tatcgaaagt ggagtatcta gcaaaacatt tacattgaca gtcttgtgat 240  
cttgaacttc ttcaattcgt aaacttaaac caatatctgg atcaatctgc aaaaacttcg 300  
actgatgcaa aattgaaaac aattcatttt ggaatcannn nnanaantna aaaaaatat 360  
atatntnttt tttttttttt ttntttnttt tttattttat cttacannac accccaacac 420  
aacacccaac ccnaaaaacac ccaacacctc catcttgtcc cgcttttctc tcacattttt 480  
tctctactac tatcacacaa tctataaaac atacaccccc tcaacccctc ctccccaaca 540  
aacctacctc cctcaactcc tatttcctcc ctcc 575

<210> 13  
<211> 921  
<212> DNA  
<213> Candida albicans

<220>  
<221> CDS  
<222> (1)..(918)

<220>  
<221> gene  
<222> (1)..(918)  
<223> gene CaOR110

<400> 13  
atg acg att gaa act att tat atc gca aga cac ggt tat aga tcc aat 48  
Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn  
1 5 10 15  
tgg tta cca cca cca cac cca cca aat cct act ggt att gac agt gac 96  
Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp  
20 25 30  
ccg gct tta gca cca cat ggt gtt gaa caa gcc caa cag tta gct gcc 144  
Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala

35	40	45	
tat ctt aca tca tta cct aca cat gaa aag cct gaa ttt att att gct Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala 50 55 60			192
tca cct ttt tat cgt tgt ata gaa acg tcg aga ccc att gcc gaa atg Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met 65 70 75 80			240
ttg gac ttg aag att gct tta gaa aga gga gtt ggt gaa tgg ttt cgt Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg 85 90 95			288
aaa aat aga gat acc aaa cca gtt ccc ggt gat tac aca caa ttg aga Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg 100 105 110			336
aca ttt ttc gat aaa tta ttg atc gat gaa gat act tgg cca aga gat Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp 115 120 125			384
aac tta aat gtt ata cct aat att gaa gga gaa gat tat gat gaa atc Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile 130 135 140			432
tac gat cgt gcc aaa ttg ttt tgg aaa aag ttt att cct gaa ttt gaa Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu 145 150 155 160			480
aag aaa ttc ccc gaa att aaa aat gtg ttg ata gtt aca cat gca gca Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala 165 170 175			528
acg aaa att gct tta gga tca gct tta tta cag tta aaa tca gtt act Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr 180 185 190			576
gat gtt ata gat gat aat caa act gtg tta cgt gct ggt gca tgt tca Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser 195 200 205			624
tta tcc aaa ttt gtt aga gat ggc gaa gat aaa acc aat cat act att Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile 210 215 220			672
caa tgg aaa att gtc atg aat ggt aat tgt gaa ttc ttg aca cag ggt Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly 225 230 235 240			720
gaa gaa atg aac tgg gat ttc cgt cgt ggt gtt gaa gcc ggg tca gct Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala 245 250 255			768
gaa gat ata gcg caa aga aag gca gca gca gaa gca gaa gca aaa gca Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala 260 265 270			816-



195	200	205
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile 210 215 220		
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly 225 230 235 240		
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala 245 250 255		
Glu Asp Ile Ala Gln Arg Lys Ala Ala Glu Ala Glu Ala Lys Ala 260 265 270		
Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser 275 280 285		
Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Val Arg 290 295 300		
Lys Thr 305		

<210> 15  
 <211> 1454  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Splice Variant

<220>  
 <221> CDS  
 <222> (1)..(1452)  
 <223> gene CaOR110 Splice Variant

<400> 15	
atg acg att gaa act att tat atc gca aga cac ggt tat aga tcc aat Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn 1 5 10 15	48
tgg tta cca cca cca cac cca cca aat cct act ggt att gac agt gac Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp 20 25 30	96
ccg gct tta gca cca cat ggt gtt gaa caa gcc caa cag tta gct gcc Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala 35 40 45	144
tat ctt aca tca tta cct aca cat gaa aag cct gaa ttt att att gct Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala 50 55 60	192
tca cct ttt tat cgt tgt ata gaa acg tcg aga ccc att gcc gaa atg Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met 65 70 75 80	240

ttg gac ttg aag att gct tta gaa aga gga gtt ggt gaa tgg ttt cgt	288
Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg	
85 90 95	
aaa aat aga gat acc aaa cca gtt ccc ggt gat tac aca caa ttg aga	336
Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg	
100 105 110	
aca ttt ttc gat aaa tta ttg atc gat gaa gat act tgg cca aga gat	384
Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp	
115 120 125	
aac tta aat gtt ata cct aat att gaa gga gaa gat tat gat gaa atc	432
Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile	
130 135 140	
tac gat cgt gcc aaa ttg ttt tgg aaa aag ttt att cct gaa ttt gaa	480
Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu	
145 150 155 160	
aag aaa ttc ccc gaa att aaa aat gtg ttg ata gtt aca cat gca gca	528
Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala	
165 170 175	
acg aaa att gct tta gga tca gct tta tta cag tta aaa tca gtt act	576
Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr	
180 185 190	
gat gtt ata gat gat aat caa act gtg tta cgt gct ggt gca tgt tca	624
Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser	
195 200 205	
tta tcc aaa ttt gtt aga gat ggc gaa gat aaa acc aat cat act att	672
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile	
210 215 220	
caa tgg aaa att gtc atg aat ggt aat tgt gaa ttc ttg aca cag ggt	720
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly	
225 230 235 240	
gaa gaa atg aac tgg gat ttc cgt cgt ggt gtt gaa gcc ggg tca gct	768
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala	
245 250 255	
gaa gat ata gcg caa aga aag gca gca gca gaa gca gaa gca aaa gca	816
Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala	
260 265 270	
ttg aag aaa aat gaa caa acc aaa tcc gat ggt ccc atc act gaa tct	864
Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser	
275 280 285	
gcc act ggg gca gaa ata gat ggg aat gaa gat gaa ttt gaa aca ttt	912
Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Thr Phe	
290 295 300	

tat gta acc atc gat ata cct tca att tcg aat aaa atc gac aat gaa	960
Tyr Val Thr Ile Asp Ile Pro Ser Ile Ser Asn Lys Ile Asp Asn Glu	
305 310 315 320	
gaa gaa cca cca tca agg aca ggt caa gct cca aaa ttc aaa aac aat	1008
Glu Glu Pro Pro Ser Arg Thr Gly Gln Ala Pro Lys Phe Lys Asn Asn	
325 330 335	
att atc aag cct tca gca caa ctc caa ttt act gat tta aaa gaa gat	1056
Ile Ile Lys Pro Ser Ala Gln Leu Gln Phe Thr Asp Leu Lys Glu Asp	
340 345 350	
cat cca tta gta aaa ata tcg aac aat act ata tct gct caa ggc tcg	1104
His Pro Leu Val Lys Ile Ser Asn Asn Thr Ile Ser Ala Gln Gly Ser	
355 360 365	
tcg tcg tcg tcg tta tca gcg tcg aaa aat gga ttt aat agt cat act	1152
Ser Ser Ser Ser Leu Ser Ala Ser Lys Asn Gly Phe Asn Ser His Thr	
370 375 380	
cac aat tca gga gtc att gat cca tca gca ctt ata gat ggg aaa att	1200
His Asn Ser Gly Val Ile Asp Pro Ser Ala Leu Ile Asp Gly Lys Ile	
385 390 395 400	
tat cag act gat tgg aat caa tta caa ggt act gaa cta ata ttt gat	1248
Tyr Gln Thr Asp Trp Asn Gln Leu Gln Gly Thr Glu Leu Ile Phe Asp	
405 410 415	
gaa aat ggt caa ttt ata ggc aag gtt aag gaa cat ttg act tgc aat	1296
Glu Asn Gly Gln Phe Ile Gly Lys Val Lys Glu His Leu Thr Cys Asn	
420 425 430	
aat aac aca aaa ttc aca tta aaa aag gca gaa gaa gta gaa caa ctt	1344
Asn Asn Thr Lys Phe Thr Leu Lys Lys Ala Glu Glu Val Glu Gln Leu	
435 440 445	
cgt tca gca gat gat tct atc atg gat ata gat caa gac tca caa gga	1392
Arg Ser Ala Asp Asp Ser Ile Met Asp Ile Asp Gln Asp Ser Gln Gly	
450 455 460	
caa caa cca gct aga agt cag ttc tta aaa aga gca att gtg gct gct	1440
Gln Gln Pro Ala Arg Ser Gln Phe Leu Lys Arg Ala Ile Val Ala Ala	
465 470 475 480	
aga gcc aaa ggt aa	1454
Arg Ala Lys Gly	

<210> 16

<211> 484

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Splice Variant

<400> 16

Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn
1 5 10 15





Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp  
 20 25 30  
 Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala  
 35 40 45  
 Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala  
 50 55 60  
 Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met  
 65 70 75 80  
 Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg  
 85 90 95  
 Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg  
 100 105 110  
 Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp  
 115 120 125  
 Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile  
 130 135 140  
 Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu  
 145 150 155 160  
 Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala  
 165 170 175  
 Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr  
 180 185 190  
 Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser  
 195 200 205  
 Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile  
 210 215 220  
 Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly  
 225 230 235 240  
 Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala  
 245 250 255  
 Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala  
 260 265 270  
 Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser  
 275 280 285  
 Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Thr Phe  
 290 295 300  
 Tyr Val Thr Ile Asp Ile Pro Ser Ile Ser Asn Lys Ile Asp Asn Glu  
 305 310 315 320

Glu Glu Pro Pro Ser Arg Thr Gly Gln Ala Pro Lys Phe Lys Asn Asn  
 325 330 335  
 Ile Ile Lys Pro Ser Ala Gln Leu Gln Phe Thr Asp Leu Lys Glu Asp  
 340 345 350  
 His Pro Leu Val Lys Ile Ser Asn Asn Thr Ile Ser Ala Gln Gly Ser  
 355 360 365  
 Ser Ser Ser Ser Leu Ser Ala Ser Lys Asn Gly Phe Asn Ser His Thr  
 370 375 380  
 His Asn Ser Gly Val Ile Asp Pro Ser Ala Leu Ile Asp Gly Lys Ile  
 385 390 395 400  
 Tyr Gln Thr Asp Trp Asn Gln Leu Gln Gly Thr Glu Leu Ile Phe Asp  
 405 410 415  
 Glu Asn Gly Gln Phe Ile Gly Lys Val Lys Glu His Leu Thr Cys Asn  
 420 425 430  
 Asn Asn Thr Lys Phe Thr Leu Lys Lys Ala Glu Glu Val Glu Gln Leu  
 435 440 445  
 Arg Ser Ala Asp Asp Ser Ile Met Asp Ile Asp Gln Asp Ser Gln Gly  
 450 455 460  
 Gln Gln Pro Ala Arg Ser Gln Phe Leu Lys Arg Ala Ile Val Ala Ala  
 465 470 475 480  
 Arg Ala Lys Gly

<210> 17  
 <211> 2877  
 <212> DNA  
 <213> Candida albicans

<220>  
 <221> CDS  
 <222> (1)..(2874)

<220>  
 <221> gene  
 <222> (1)..(2874)  
 <223> gene CaMR212

<400> 17  
 atg aat ttg ttt caa cat aaa cat caa aaa tta ata tta caa tgt tat 48  
 Met Asn Leu Phe Gln His Lys His Gln Lys Leu Ile Leu Gln Cys Tyr  
 1 5 10 15

cct gct ggg aaa gca gtg gac aaa aaa ccc aac tcg tcc gag tta agt 96  
 Pro Ala Gly Lys Ala Val Asp Lys Lys Pro Asn Ser Ser Glu Leu Ser  
 20 25 30

tat tta tta tac tat gca tcc act cgt aga gtc aaa tta gaa aag gtg	144
Tyr Leu Leu Tyr Tyr Ala Ser Thr Arg Arg Val Lys Leu Glu Lys Val	
35 40 45	
att aat ttt ttg aaa gat aaa act cat cat gat gtt ggt aga aac cgt	192
Ile Asn Phe Leu Lys Asp Lys Thr His His Asp Val Gly Arg Asn Arg	
50 55 60	
act ggt aat tta caa gtc aca tta gcc att att cag gaa tta atc aaa	240
Thr Gly Asn Leu Gln Val Thr Leu Ala Ile Ile Gln Glu Leu Ile Lys	
65 70 75 80	
aaa tgt agt gaa aac ttg aat gtt ttt gcc ttt caa gtg tgc tat atc	288
Lys Cys Ser Glu Asn Leu Asn Val Phe Ala Phe Gln Val Cys Tyr Ile	
85 90 95	
ttg caa ctg att gcc aac act aag gat ctt gcc ttg tgt aaa aat gtt	336
Leu Gln Leu Ile Ala Asn Thr Lys Asp Leu Ala Leu Cys Lys Asn Val	
100 105 110	
gtc aaa aca ttt ggt gtt ttg tgt gaa aac ttg gat ggt ggg ttg ttc	384
Val Lys Thr Phe Gly Val Leu Cys Glu Asn Leu Asp Gly Gly Leu Phe	
115 120 125	
aca ggt gat aag gag ttt ata aag att ttc act gaa gtt ttc caa aca	432
Thr Gly Asp Lys Glu Phe Ile Lys Ile Phe Thr Glu Val Phe Gln Thr	
130 135 140	
tta gtt tcc ttt ggt aag gac aga tcg ggt gtt act cag tat gat tgg	480
Leu Val Ser Phe Gly Lys Asp Arg Ser Gly Val Thr Gln Tyr Asp Trp	
145 150 155 160	
cag atg att tct tta atg gct ata aat gat ata tcc agt tgt ttg agt	528
Gln Met Ile Ser Leu Met Ala Ile Asn Asp Ile Ser Ser Cys Leu Ser	
165 170 175	
tat aat gca gct gtt ggt aaa aag ttt att gct ttg tcg att cct gtt	576
Tyr Asn Ala Ala Val Gly Lys Lys Phe Ile Ala Leu Ser Ile Pro Val	
180 185 190	
tta ctt cag ttt att att gca aac aac cca caa agc agc ata ttg caa	624
Leu Leu Gln Phe Ile Ile Ala Asn Asn Pro Gln Ser Ser Ile Leu Gln	
195 200 205	
aga ttg aaa tcg aat ctc cac gtt gaa gat gat ggg aag agg ttg tca	672
Arg Leu Lys Ser Asn Leu His Val Glu Asp Asp Gly Lys Arg Leu Ser	
210 215 220	
cgt gct cat ctg caa aaa tcc cat agc aaa att gcc caa caa att gat	720
Arg Ala His Leu Gln Lys Ser His Ser Lys Ile Ala Gln Gln Ile Asp	
225 230 235 240	
gat gat ttc acc aat gat tct tta acc ttg aca gat atc act gaa aag	768
Asp Asp Phe Thr Asn Asp Ser Leu Thr Leu Thr Asp Ile Thr Glu Lys	
245 250 255	
gca ttt tcg tcg atg aaa tct ttt ttc aat acc aat gct gcc agt caa	816

Ala Phe Ser Ser Met Lys Ser Phe Phe Asn Thr Asn Ala Ala Ser Gln	
260 265 270	
atc tct gaa gtg aca aga gct gtt gtc caa cac aat att ctc aat gga	864
Ile Ser Glu Val Thr Arg Ala Val Val Gln His Asn Ile Leu Asn Gly	
275 280 285	
acc gat ttg gag tgg gga gtc tca ttc ttg gaa tta tgt att act tgg	912
Thr Asp Leu Glu Trp Gly Val Ser Phe Leu Glu Leu Cys Ile Thr Trp	
290 295 300	
att cca gtt caa tta cgt ttt gtc agt ttg tcc acc ttg ttg gcc act	960
Ile Pro Val Gln Leu Arg Phe Val Ser Leu Ser Thr Leu Leu Ala Thr	
305 310 315 320	
tta ggt aga att aat att gaa ggt aac acc aaa tcc aat tac aac atg	1008
Leu Gly Arg Ile Asn Ile Glu Gly Asn Thr Lys Ser Asn Tyr Asn Met	
325 330 335	
caa ttc cag tat gct cgt tac ttg tta gga tta ctt tca tct cgt gtg	1056
Gln Phe Gln Tyr Ala Arg Tyr Leu Leu Gly Leu Leu Ser Ser Arg Val	
340 345 350	
aac atg att ggg tta tca gtt tca gat att att caa cag ttg tta tcg	1104
Asn Met Ile Gly Leu Ser Val Ser Asp Ile Ile Gln Gln Leu Leu Ser	
355 360 365	
ttg caa gct gat ttg att ttg aag gca agt gat ttg gac aaa agt gaa	1152
Leu Gln Ala Asp Leu Ile Leu Lys Ala Ser Asp Leu Asp Lys Ser Glu	
370 375 380	
att tca att tta aca gac att tat tct gac tgt att tgt agt ttg act	1200
Ile Ser Ile Leu Thr Asp Ile Tyr Ser Asp Cys Ile Cys Ser Leu Thr	
385 390 395 400	
aca cat ata tat tac ttt gat caa gtc ccg gac tcg att caa gaa atc	1248
Thr His Ile Tyr Tyr Phe Asp Gln Val Pro Asp Ser Ile Gln Glu Ile	
405 410 415	
tta atc aag att gat tac att tta gaa agc agt ttt gtg gaa gat aat	1296
Leu Ile Lys Ile Asp Tyr Ile Leu Glu Ser Ser Phe Val Glu Asp Asn	
420 425 430	
aac att acg tcc act gga gaa caa att caa gat ttg att atc caa ttg	1344
Asn Ile Thr Ser Thr Gly Glu Gln Ile Gln Asp Leu Ile Ile Gln Leu	
435 440 445	
ttg gat aac att tcg aag att ttt tta att ttg aag aat aaa tca agc	1392
Leu Asp Asn Ile Ser Lys Ile Phe Leu Ile Leu Lys Asn Lys Ser Ser	
450 455 460	
tca att aat cgt aac cat gtg aat ttg gaa cat tgg gat atc agt tta	1440
Ser Ile Asn Arg Asn His Val Asn Leu Glu His Trp Asp Ile Ser Leu	
465 470 475 480	
gga tta ttg gct cca caa ggc gac cat gat gat aac aga aaa atg att	1488
Gly Leu Leu Ala Pro Gln Gly Asp His Asp Asp Asn Arg Lys Met Ile	